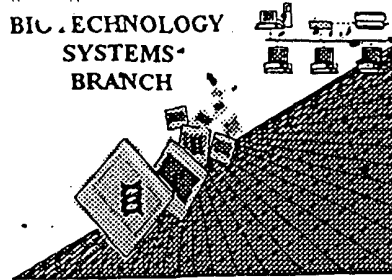


0590
10/23

BIO. TECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/900 425

Source: O I P E

Date Processed by STIC: 11/13/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/900425

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length.** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence.
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/900,425

DATE: 11/13/2001

TIME: 09:58:53

Input Set : A:\isph522.mh.pto.txt

Output Set: N:\CRF3\11092001\I900425.raw

3 <110> APPLICANT: Wu, Hongjiang
 4 Crooke, Stanley T.
 6 <120> TITLE OF INVENTION: Human RNase III and Compositions and Uses Thereof
 8 <130> FILE REFERENCE: ISPH-0522
 W--> 9 <140> CURRENT APPLICATION NUMBER: US 09/900,425
 10 <141> CURRENT FILING DATE: 2001-07-06
 12 <150> PRIOR APPLICATION NUMBER: US 09/479,783
 13 <151> PRIOR FILING DATE: 2000-01-07
 15 <150> PRIOR APPLICATION NUMBER: US 08/870,608
 16 <151> PRIOR FILING DATE: 1997-06-06
 18 <150> PRIOR APPLICATION NUMBER: US 80/659,440
 19 <151> PRIOR FILING DATE: 1996-06-06
 21 <160> NUMBER OF SEQ ID NOS: 36
 23 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply
 Corrected Diskette Needed

Does Not Comply
 Corrected Diskette Needed

ERRORS

192 <210> SEQ ID NO: 2
 193 <211> LENGTH: 1374
 194 <212> TYPE: PRT
 195 <213> ORGANISM: Homo sapiens
 197 <400> SEQUENCE: 2

199 Met Met Gln Gly Asn Thr Cys His Arg Met Ser Phe His Pro Gly Arg
 200 1 5 10 15
 202 Gly Cys Pro Arg Gly Arg Gly Gly His Gly Ala Arg Pro Ser Ala Pro
 203 20 25 30
 205 Ser Phe Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro
 206 35 40 45
 208 Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser
 209 50 55 60
 211 Asn Ser Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro
 212 65 70 75 80
 214 Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys
 215 85 90 95
 217 Pro Ile Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro
 218 100 105 110
 220 Val Pro Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn
 221 115 120 125
 223 Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe
 224 130 135 140
 226 Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Val Met
 227 145 150 155 160
 229 Pro Gln Gln Val Asn Tyr Gln Tyr Pro Pro Gly Tyr Ser His His Asn
 230 165 170 175
 232 Phe Pro Pro Pro Ser Phe Asn Ser Phe Gln Asn Asn Pro Ser Ser Phe
 233 180 185 190

Errors:

1. not aligned amino numbering see pages 4 and 5
 2. Invalid 213 response see page 5 of 813

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/900,425

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TIME: 09:58:53

Input Set : A:\isph522.mh.pto.txt

Output Set: N:\CRF3\11092001\I900425.raw

```

235 Leu Pro Ser Ala Asn Asn Ser Ser Ser Pro His Phe Arg His Leu Pro
236          195          200          205
238 Pro Tyr Pro Leu Pro Lys Ala Pro Ser Glu Arg Arg Ser Pro Glu Arg
239          210          215          220
241 Leu Lys His Tyr Asp Asp His Arg His Arg Asp His Ser His Gly Arg
242 225          230          235          240
244 Gly Glu Arg His Arg Ser Leu Asp Arg Arg Glu Arg Gly Arg Ser Pro
245          245          250          255
247 Asp Arg Arg Arg Gln Asp Ser Arg Tyr Arg Ser Asp Tyr Asp Arg Gly
248          260          265          270
250 Arg Thr Pro Ser Arg His Arg Ser Tyr Glu Arg Ser Arg Glu Arg Glu
251          275          280          285
253 Arg Glu Arg His Arg His Arg Asp Asn Arg Arg Ser Pro Ser Leu Glu
254          290          295          300
256 Arg Ser Tyr Lys Lys Glu Tyr Lys Arg Ser Gly Arg Ser Tyr Gly Leu
257 305          310          315          320
259 Ser Val Val Pro Glu Pro Ala Gly Cys Thr Pro Glu Leu Pro Gly Glu
260          325          330          335
262 Ile Ile Lys Asn Thr Asp Ser Trp Ala Pro Pro Leu Glu Ile Val Asn
263          340          345          350
265 His Arg Ser Pro Ser Arg Glu Lys Lys Arg Ala Arg Trp Glu Glu Glu
266          355          360          365
268 Lys Asp Arg Trp Ser Asp Asn Gln Ser Ser Gly Lys Asp Lys Asn Tyr
269          370          375          380
271 Thr Ser Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn
272 385          390          395          400
274 Glu Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
275          405          410          415
277 His Ser Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp
278          420          425          430
280 Ser Thr Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe
281          435          440          445
283 Glu Glu Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro
284          450          455          460
286 Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
287 465          470          475          480
289 Ser Glu Ser Glu Cys Glu Ser Asp Glu Asp Ser Thr Cys Ser Ser Ser
290          485          490          495
292 Ser Asp Ser Glu Val Phe Asp Val Ile Ala Glu Ile Lys Arg Lys Lys
293          500          505          510
295 Ala His Pro Asp Arg Leu His Asp Glu Leu Trp Tyr Asn Asp Pro Gly
296          515          520          525
298 Gln Met Asn Asp Gly Pro Leu Cys Lys Cys Ser Ala Lys Ala Arg Arg
299          530          535          540
301 Thr Gly Ile Arg His Ser Ile Tyr Pro Gly Glu Glu Ala Ile Lys Pro
302 545          550          555          560
304 Cys Arg Pro Met Thr Asn Asn Ala Gly Arg Leu Phe His Tyr Arg Ile
305          565          570          575
307 Thr Val Ser Pro Pro Thr Asn Phe Leu Thr Asp Arg Pro Thr Val Ile

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/900,425

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Input Set : A:\isph522.mh.pto.txt

Output Set: N:\CRF3\11092001\I900425.raw

308				580					585				590			
310	Glu	Tyr	Asp	Asp	His	Glu	Tyr	Ile	Phe	Glu	Gly	Phe	Ser	Met	Phe	Ala
311			595					600					605			
313	His	Ala	Pro	Leu	Thr	Asn	Ile	Pro	Leu	Cys	Lys	Val	Ile	Arg	Phe	Asn
314		610					615					620				
316	Ile	Asp	Tyr	Thr	Ile	His	Phe	Ile	Glu	Glu	Met	Met	Pro	Glu	Asn	Phe
317	625					630					635				640	
319	Cys	Val	Lys	Gly	Leu	Glu	Leu	Phe	Ser	Leu	Phe	Leu	Phe	Arg	Asp	Ile
320				645					650					655		
322	Leu	Glu	Leu	Tyr	Asp	Trp	Asn	Leu	Lys	Gly	Pro	Leu	Phe	Glu	Asp	Ser
323			660					665					670			
325	Pro	Pro	Cys	Cys	Pro	Arg	Phe	His	Phe	Met	Pro	Arg	Phe	Val	Arg	Phe
326			675				680						685			
328	Leu	Pro	Asp	Gly	Gly	Lys	Glu	Val	Leu	Ser	Met	His	Gln	Ile	Leu	Leu
329		690				695					700					
331	Tyr	Leu	Leu	Arg	Cys	Ser	Lys	Ala	Leu	Val	Pro	Glu	Glu	Glu	Ile	Ala
332	705					710					715				720	
334	Asn	Met	Leu	Gln	Trp	Glu	Glu	Leu	Glu	Trp	Gln	Lys	Tyr	Ala	Glu	Glu
335				725					730						735	
337	Cys	Lys	Gly	Met	Ile	Val	Thr	Asn	Pro	Gly	Thr	Lys	Pro	Ser	Ser	Val
338			740					745					750			
340	Arg	Ile	Asp	Gln	Leu	Asp	Arg	Glu	Gln	Phe	Asn	Pro	Asp	Val	Ile	Thr
341			755				760						765			
343	Phe	Pro	Ile	Ile	Val	His	Phe	Gly	Ile	Arg	Pro	Ala	Gln	Leu	Ser	Tyr
344		770					775					780				
346	Ala	Gly	Asp	Pro	Gln	Tyr	Gln	Lys	Leu	Trp	Lys	Ser	Tyr	Val	Lys	Leu
347	785					790					795				800	
349	Arg	His	Leu	Leu	Ala	Asn	Ser	Pro	Lys	Val	Lys	Gln	Thr	Asp	Lys	Gln
350				805					810						815	
352	Lys	Leu	Ala	Gln	Arg	Glu	Glu	Ala	Leu	Gln	Lys	Ile	Arg	Gln	Lys	Asn
353			820					825					830			
355	Thr	Met	Arg	Arg	Glu	Val	Thr	Val	Glu	Leu	Ser	Ser	Gln	Gly	Phe	Trp
356			835				840						845			
358	Lys	Thr	Gly	Ile	Arg	Ser	Asp	Val	Cys	Gln	His	Ala	Met	Met	Leu	Pro
359		850				855					860					
361	Val	Leu	Thr	His	His	Ile	Arg	Tyr	His	Gln	Cys	Leu	Met	His	Leu	Asp
362	865					870				875					880	
364	Lys	Leu	Ile	Gly	Tyr	Thr	Phe	Gln	Asp	Arg	Cys	Leu	Leu	Gln	Leu	Ala
365				885					890						895	
367	Met	Thr	His	Pro	Ser	His	His	Leu	Asn	Phe	Gly	Met	Asn	Pro	Asp	His
368			900					905						910		
370	Ala	Arg	Asn	Ser	Leu	Ser	Asn	Cys	Gly	Ile	Arg	Gln	Pro	Lys	Tyr	Gly
371			915				920						925			
373	Asp	Arg	Lys	Val	His	His	Met	His	Met	Arg	Lys	Lys	Gly	Ile	Asn	Thr
374		930				935						940				
376	Leu	Ile	Asn	Ile	Met	Ser	Arg	Leu	Gly	Gln	Asp	Asp	Pro	Thr	Pro	Ser
377	945					950					955				960	
379	Arg	Ile	Asn	His	Asn	Glu	Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Val	Val
380				965					970						975	

RAW SEQUENCE LISTING

DATE: 11/13/2001

PATENT APPLICATION: US/09/900,425

TIME: 09:58:53

Input Set : A:\isph522.mh.pto.txt

Output Set: N:\CRF3\11092001\I900425.raw

```

382 Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
383                               980                               985                               990
385 Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln Asn Gln His
386                               995                               1000                               1005
388 Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro Phe Met Leu Tyr
389                               1010                               1015                               1020
391 Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg His Ala Met
392 1025                               1030                               1035                               1040
394 Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu Glu Gly Ser
395                               1045                               1050                               1055
397 Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe Asn Asp Pro
398                               1060                               1065                               1070
400 Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro Leu Gln Leu
401                               1075                               1080                               1085
403 Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser Pro Val Leu
404                               1090                               1095                               1100
406 Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile Phe Thr His
407 1105                               1110                               1115                               1120
409 Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val Gly Phe Asn
410                               1125                               1130                               1135
412 His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu Gly Asp Ser
413                               1140                               1145                               1150
415 Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile His Phe Pro Asp
416                               1155                               1160                               1165
418 His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser Leu Val Asn Asn
419                               1170                               1175                               1180
421 Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met Gln Glu Tyr Ala
422 1185                               1190                               1195                               1200
424 Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu Arg Thr Lys Thr
425                               1205                               1210                               1215
427 Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu Tyr Thr Asp Lys
428                               1220                               1225                               1230
430 Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys Phe Phe Pro Arg
E--> 431 1235 1240 1245
433 Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp Pro Lys Ser Gln
E--> 434 1250 1255 1260 1265
436 Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly Lys Glu Pro Asp
E--> 437 1270 1275 1280
439 Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro Ser His Ala Arg
E--> 440 1285 1290 1295
442 Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg Ile Gly Cys Gly
E--> 443 1300 1305 1310
445 Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala Ala Met Asp Ala
E--> 446 1315 1320 1325
448 Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln Lys Arg Phe Ile
E--> 449 1330 1335 1340 1345
451 Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg Trp Glu Arg Glu
E--> 452 1350 1355 1360
455 His Gln Glu Arg Glu Pro Asp Glu Thr Glu Asp Ile Lys Lys

```

② + number should be under 1st letter

① * Error - From 1230 to 1235 are only 4 amino representations.

RAW SEQUENCE LISTING

DATE: 11/13/2001

PATENT APPLICATION: US/09/900,425

TIME: 09:58:53

Input Set : A:\isph522.mh.pto.txt

Output Set: N:\CRF3\11092001\I900425.raw

E--> 456 1365 1370

③ amino numbering should be
separated by five amino
triplet & abbreviations

<210> 8

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Synthetic

<400> 8

atccctttct tccgatgtg

Preferred Terminology
is "Artificial Sequence"

This type of error exists
throughout²⁰ the sequence listing.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

"Artificial" is an invalid 213 response
"Artificial Sequence" is preferred.

VERIFICATION SUMMARY

DATE: 11/13/2001

PATENT APPLICATION: US/09/900,425

TIME: 09:58:54

Input Set : A:\isph522.mh.pto.txt

Output Set: N:\CRF3\11092001\I900425.raw

L:9 M:283 W: Missing Blank Line separator, <140> field identifier
L:431 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:787 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:788 M:283 W: Missing Blank Line separator, <220> field identifier
L:798 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:799 M:283 W: Missing Blank Line separator, <220> field identifier
L:809 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:810 M:283 W: Missing Blank Line separator, <220> field identifier
L:820 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:821 M:283 W: Missing Blank Line separator, <220> field identifier
L:831 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:832 M:283 W: Missing Blank Line separator, <220> field identifier
L:842 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:843 M:283 W: Missing Blank Line separator, <220> field identifier
L:853 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:854 M:283 W: Missing Blank Line separator, <220> field identifier
L:864 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:865 M:283 W: Missing Blank Line separator, <220> field identifier
L:875 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:876 M:283 W: Missing Blank Line separator, <220> field identifier
L:885 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:897 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:898 M:283 W: Missing Blank Line separator, <220> field identifier
L:908 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:909 M:283 W: Missing Blank Line separator, <220> field identifier
L:919 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:920 M:283 W: Missing Blank Line separator, <220> field identifier
L:930 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:931 M:283 W: Missing Blank Line separator, <220> field identifier
L:941 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:942 M:283 W: Missing Blank Line separator, <220> field identifier
L:952 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:953 M:283 W: Missing Blank Line separator, <220> field identifier
L:963 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:964 M:283 W: Missing Blank Line separator, <220> field identifier
L:974 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:975 M:283 W: Missing Blank Line separator, <220> field identifier
L:985 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:986 M:283 W: Missing Blank Line separator, <220> field identifier
L:996 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:997 M:283 W: Missing Blank Line separator, <220> field identifier
L:1007 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:1008 M:283 W: Missing Blank Line separator, <220> field identifier
L:1018 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:1019 M:283 W: Missing Blank Line separator, <220> field identifier
L:1029 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:1030 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,425

DATE: 11/13/2001

TIME: 09:58:54

Input Set : A:\isph522.mh.pto.txt

Output Set: N:\CRF3\11092001\I900425.raw

L:1040 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:1041 M:283 W: Missing Blank Line separator, <220> field identifier
L:1051 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:1052 M:283 W: Missing Blank Line separator, <220> field identifier
L:1062 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:1063 M:283 W: Missing Blank Line separator, <220> field identifier
L:1073 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:1074 M:283 W: Missing Blank Line separator, <220> field identifier